



SEQUENCE LISTING

<110> Saxon, Andrew

<120> FUSION MOLECULES AND METHODS FOR
TREATMENT OF IMMUNE DISEASES

<130> UC067.004A

<140> US 10/000,439
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<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 696

<212> DNA

<213> Homo sapiens

<400> 1

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gggggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccg 120
acccctgagg tcacatgcgt ggtgggac gtgagccacg aagaccctga ggtcaagttc 180
aactggtagc tgacggcgt ggaggtgcat aatgttaaga caaagcccg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagaa ctggatgaat 300
ggaaaaggagt acaagtgcac ggtctccaac aaagccctcc cagccccat cgagaaaaacc 360
atctccaaag ccaaagtgca gccccgagaa ccacaggtgt acaccctgcc cccatcccg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccggtctgg actccgtcgg ctccttcttc ctctacagca agctaccgt ggacaagagc 600
aggtgtccgc aggggaacgt cttctcatgc tccgtatgc atgaggctct gcacaaccac 660
taccagcaga ggagcctctc cctgtctccg ggtaaa 696

<210> 2

<211> 330

<212> PRT

<213> Homo sapiens

<400> 2

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys
1				5				10					15		
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
					20			25					30		
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
					35			40					45		
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
					50			55					60		
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
					65			70					75		80
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
					85			90					95		
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
					100			105					110		
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	

115	120	125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys		
130	135	140
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp		
145	150	155
Tyr Val Asp Gly Val Glu Val His Asn Val Lys Thr Lys Pro Arg Glu		160
165	170	175
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu		
180	185	190
His Gln Asn Trp Met Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn		
195	200	205
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Val		
210	215	220
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu		
225	230	235
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr		240
245	250	255
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn		
260	265	270
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Val Gly Ser Phe Phe		
275	280	285
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn		
290	295	300
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Gln		
305	310	315
Gln Arg Ser Leu Ser Leu Ser Pro Gly Lys		320
325	330	

<210> 3
 <211> 232
 <212> PRT
 <213> Homo sapiens

<400> 3

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala			
1	5	10	15
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro			
20	25	30	
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val			
35	40	45	
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val			
50	55	60	
Asp Gly Val Glu Val His Asn Val Lys Thr Lys Pro Arg Glu Glu Gln			
65	70	75	80
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln			
85	90	95	
Asn Trp Met Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala			
100	105	110	
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Val Gln Pro			
115	120	125	
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr			
130	135	140	
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser			
145	150	155	160
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr			
165	170	175	
Lys Thr Thr Pro Pro Val Leu Asp Ser Val Gly Ser Phe Phe Leu Tyr			
180	185	190	
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe			
195	200	205	

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Gln Gln Arg
210 215 220
Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 4
<211> 1445
<212> DNA
<213> Homo sapiens

<400> 4
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acctggaca caggctccct caacggaca actatgaccc taccagccac caccctcag 180
ctctctggc actatgccac catcagctt ctgaccgtc cgggtgcgtg ggccaagcag 240
atgttcacct gccgtgtggc acacactcca tcgtccacag actgggtcga caacaaaacc 300
ttcagcgtct gctccaggga cttcaccccg cccaccgtga agatcttaca gtcgtcctgc 360
gacggccggc ggcacttccc cccgaccatc cagctcctgt gcctcgtctc tgggtacacc 420
ccagggacta tcaacatcac ctggctggag gacgggcagg tcatggacgt ggacttgc 480
accgcctcta ccacgcagga gggtagctg gcctccacac aaagcgagct caccctcagc 540
cagaagact ggctgtcaga ccgcacccatc acctgccagg tcacctatca aggtcacacc 600
tttgaggaca gcaccaagaa gtgtgcagat tccaacccga gagggtgag cgcctaccta 660
agccggccca gcccggttca gctgttcatc cgcaagtcgc ccacgatcac ctgtctgg 720
gtggacttgg caccctggaa ggggaccgtg aacctgaccc ggtccggc cagtggaaag 780
cctgtgaacc actccaccag aaaggaggag aagcagcgc atggcacgtt aaccgtcagc 840
tccaccctgc cggtggcac ccgcagactgg atcgaggggg agacccatca gtcaggggtg 900
accacccccc actgcggccag ggcctcatc cggtccacca ccaagaccag cggcccggt 960
gctggcccg aagtctatgc gtttgcacg ccggagtgcc cggggagccg ggacaagcgc 1020
accctcgccct gcctgatcca gaacttcatc cctgaggaca tctcggtca gtggctgcac 1080
aacgagggtc agctcccgga cgcggcac agcagcgc agcccccga gaccaaggc 1140
tccggcttct tcgttcttca ggcctggag gtgaccaggg ccgaatggga gcagaaagat 1200
gagttcatct gccgtgcagt ccatgaggca gcgagccct cacagaccgt ccagcgcgc 1260
gtgtctgtaa atcccggtaa atgacgtact cctgcctccc tccctccag ggctccatcc 1320
agctgtgcag tggggaggac tggccagacc ttctgtccac tggtaatg accccaggaa 1380
gctacccca ataaactgtg cctgctcaga gcccagtagc acccatttcc gggagcggc 1440
aggc 1445

<210> 5
<211> 427
<212> PRT
<213> Homo sapiens

<400> 5
Ser Thr Gln Ser Pro Ser Val Phe Pro Leu Thr Arg Cys Cys Lys Asn
1 5 10 15
Ile Pro Ser Asn Ala Thr Ser Val Thr Leu Gly Cys Leu Ala Thr Gly
20 25 30
Tyr Phe Pro Glu Pro Val Met Val Thr Trp Asp Thr Gly Ser Leu Asn
35 40 45
Gly Thr Thr Met Thr Leu Pro Ala Thr Thr Leu Thr Leu Ser Gly His
50 55 60
Tyr Ala Thr Ile Ser Leu Leu Thr Val Ser Gly Ala Trp Ala Lys Gln
65 70 75 80
Met Phe Thr Cys Arg Val Ala His Thr Pro Ser Ser Thr Asp Trp Val
85 90 95
Asp Asn Lys Thr Phe Ser Val Cys Ser Arg Asp Phe Thr Pro Pro Thr
100 105 110
Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly His Phe Pro Pro
115 120 125
Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile

130	135	140
Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser		
145	150	155
Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu		160
165	170	175
Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr Cys		
180	185	190
Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys Cys		
195	200	205
Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro Ser		
210	215	220
Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu Val		
225	230	235
Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser Arg		240
245	250	255
Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys Gln		
260	265	270
Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr Arg		
275	280	285
Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro His		
290	295	300
Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser Gly Pro Arg		
305	310	315
Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp Pro Gly Ser		320
325	330	335
Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn Phe Met Pro Glu		
340	345	350
Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu Pro Asp Ala		
355	360	365
Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser Gly Phe Phe		
370	375	380
Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu Gln Lys Asp		
385	390	395
Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro Ser Gln Thr		400
405	410	415
Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys		
420	425	

<210> 6
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 6
 Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly
 1 5 10 15
 Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr
 20 25 30
 Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met
 35 40 45
 Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala
 50 55 60
 Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp
 65 70 75 80
 Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp
 85 90 95
 Ser Thr Lys Lys Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr
 100 105 110
 Leu Ser Arg Pro Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr
 115 120 125

Ile Thr Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn
130 135 140
Leu Thr Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg
145 150 155 160
Lys Glu Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu
165 170 175
Pro Val Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg
180 185 190
Val Thr His Pro His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys
195 200 205
Thr Ser Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro
210 215 220
Glu Trp Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln
225 230 235 240
Asn Phe Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val
245 250 255
Gln Leu Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys
260 265 270
Gly Ser Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu
275 280 285
Trp Glu Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala
290 295 300
Ser Pro Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
305 310 315 320

<210> 7
<211> 569
<212> PRT
<213> Unknown

<220>
<223> Fusion polypeptide comprising a hinge-CH2-CH3
(IgG1) sequence and a CH2-CH3-CH4 (IgE) sequence

<400> 7
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60
Asp Gly Val Glu Val His Asn Val Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95
Asn Trp Met Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Val Gln Pro
115 120 125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175
Lys Thr Thr Pro Pro Val Leu Asp Ser Val Gly Ser Phe Phe Leu Tyr
180 185 190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe

195	200	205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Gln Gln Arg		
210	215	220
Ser Leu Ser Leu Ser Pro Gly Lys Val Glu Gly Gly Gly Ser Gly		
225	230	235
Gly Gly Gly Ser Gly Gly Gly Ser Phe Thr Pro Pro Thr Val Lys		
245	250	255
Ile Leu Gln Ser Ser Cys Asp Gly Gly His Phe Pro Pro Thr Ile		
260	265	270
Gln Leu Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile Asn Ile		
275	280	285
Thr Trp Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser Thr Ala		
290	295	300
Ser Thr Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu Leu Thr		
305	310	315
Leu Ser Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr Cys Gln Val		
325	330	335
Thr Tyr Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys Cys Ala Asp		
340	345	350
Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro Ser Pro Phe		
355	360	365
Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu Val Val Asp		
370	375	380
Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser Arg Ala Ser		
385	390	395
Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys Gln Arg Asn		
405	410	415
Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr Arg Asp Trp		
420	425	430
Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro His Leu Pro		
435	440	445
Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser Gly Pro Arg Ala Ala		
450	455	460
Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp Pro Gly Ser Arg Asp		
465	470	475
Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn Phe Met Pro Glu Asp Ile		
485	490	495
Ser Val Gln Trp Leu His Asn Glu Val Gln Leu Pro Asp Ala Arg His		
500	505	510
Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser Gly Phe Phe Val Phe		
515	520	525
Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu Gln Lys Asp Glu Phe		
530	535	540
Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro Ser Gln Thr Val Gln		
545	550	555
Arg Ala Val Ser Val Asn Pro Gly Lys		
565		

<210> 8
 <211> 73
 <212> DNA
 <213> Unknown

<220>
 <223> primer sequence

<400> 8
 gctcgagggt ggaggcggtt caggcgagg tggctctggc ggtggcggat cgttcacccc 60
 gcccaccgtg aag 73

<210> 9
<211> 33
<212> DNA
<213> Unknown

<220>
<223> primer sequence

<400> 9
ggcggccgct catttacccgg gatttacaga cac

33

<210> 10
<211> 32
<212> PRT
<213> Arachis hypogaea (peanut)

<220>
<221> UNSURE
<222> 1, 4, 11, 12, 27, 30
<223> Xaa = any amino acid

<400> 10
Xaa Gln Gln Xaa Glu Leu Gln Asp Leu Glu Xaa Xaa Gln Ser Gln Leu
1 5 10 15
Glu Asp Ala Asn Leu Arg Pro Arg Glu Gln Xaa Leu Met Xaa Lys Ile
20 25 30

<210> 11
<211> 32
<212> PRT
<213> Arachis hypogaea (peanut)

<220>
<221> UNSURE
<222> 1, 4, 8, 10, 11, 12, 27, 30
<223> Xaa = any amino acid

<400> 11
Xaa Gln Gln Xaa Glu Leu Gln Xaa Asp Xaa Xaa Gln Ser Gln Leu
1 5 10 15
Glu Arg Ala Asp Leu Arg Pro Gly Glu Gln Xaa Leu Met Xaa Lys Ile
20 25 30

<210> 12
<211> 171
<212> PRT
<213> Homo sapiens

<400> 12
Met Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu
1 5 10 15
Ala Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg
20 25 30
His Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly
35 40 45
Asp Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Pro
50 55 60
Ala Arg Thr Ala His Tyr Gly Ser Leu Pro Gln Lys Ser His Gly Arg
65 70 75 80

Thr Gln Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr
85 90 95
Pro Arg Thr Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu
100 105 110
Ser Arg Phe Ser Trp Gly Ala Glu Gly Gln Arg Pro Gly Phe Gly Tyr
115 120 125
Gly Gly Arg Ala Ser Asp Tyr Lys Ser Ala His Lys Gly Phe Lys Gly
130 135 140
Val Asp Ala Gln Gly Thr Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg
145 150 155 160
Asp Ser Arg Ser Gly Ser Pro Met Ala Arg Arg
165 170

<210> 13
<211> 17
<212> PRT
<213> Homo sapiens

<400> 13
Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg Thr
1 5 10 15
Pro